In the Specification:

In the specification, please make the following amendments:

In ¶ [0027]

[0027] In one preferred embodiment of the invention, a peptide is prepared that comprises R1-Lys-X1-Val (SEQ. ID. NO. 1), where Val is the carboxy-terminal amino acid and X1 is either Phe or DPhe and where R1 is His-Phe-Arg-Trp-Gly. In another preferred embodiment of the invention, a peptide is prepared that contains His-X2-Arg-Trp-Gly-Lys-Pro-Val (SEQ. ID. NO. 2), where X2 is, D-Phe, or DNle[[al]]. This can be combined with SEQ. ID NO. 1 via a Gly-Lys bond giving His-X2-Arg-Trp-Gly-Lsy-X1-Val (SEQ. ID NO. 3.) Here, the sequences are connected through a Gly-Lys peptide bond resulting in a peptide where Val is the carboxy-terminal amino acid.

In ¶ [0032]

[0032] In another preferred embodiment of the invention, a peptide is prepared consisting of R1-Lys-X7-Val (SEQ. ID. NO. 8) where Val is the carboxy-terminal amino acid and where X7 is an amino acid having a negatively charged functional group. Negatively charged functional group amino acids may be selected from the group consisting of Asp, Glu, and their D-isomers thereof. In another preferred embodiment of the invention, a peptide is prepared where SEQ. ID NO. 2, His-X2-Arg-Trp-Gly is connected to the Lys of SEQ. ID NO. 8, giving His-X2-Arg-Trp-Gly-Lys-X7-Val (SEQ. ID. NO. 9), and where X2, as above, is DPhe or DNle[[al]]. Similar to above, SEQ. ID NO. 2 and SEQ. ID NO. 7 are connected via a Gly-Lys.. In other words, SEQ. ID NO. 2 replaces the R1 in SEQ. ID NO. 7.

In ¶ [0058]

[0058] Replacing the Phe residue within the His-Phe-Arg sequence with DNle[[al]] resulted in increased activity in almost all peptides tested, confirming a behavior found previously in melanocortin peptides.

Please amend Table 1 as follows:

Table 1

SEQ. ID NO.	Structure	% Inhib.	SD
18	His-Phe-Arg-Trp-Gly-Lys-Pro-*Dval*	82.5	26.8
19	His-Phe-Arg-Trp-Gly-*Ala*-Pro-Val	26.2	29.1
20	His-Phe-Arg-Trp-Gly-Lys-*Ala*-Val	12.8	18.1
21	His-Phe-Arg-Trp-Gly-Lys-Pro-*Ala*	68.4	31.5
22	His-*DPhe*-Arg-Trp-Gly-Lys-Pro-Val	79.4	27.3
23	His-DNle[[al]]-Arg-Trp-Gly-Lys-Pro-Val	95.3	7.7
24	His-Phe-Arg-*DTrp*-Gly-Lys-Pro-Val	81.9	24.5
25	His-Phe-Arg-Trp-Gly-Lys-Pro-*Leu*	86.6	23.2
26	His-Phe-Arg-Trp-Gly-Lys-*DAla*-Val	43.7	29.5
27	His-DNle[[al]]-Arg-Trp-Gly-Lys-*Ala*-Val	28.0	24.5
28	His-DNle[[al]]-Arg-Trp-Gly-Lys-*DAla*-Val	69.2	27.1
29	His-Phe-Arg-Trp-Gly-Lys-*Gly*-Val	41.8	27.9
30	His-DNle[[al]]-Arg-Trp-Gly-Lys-*Gly*-Val	36.2	24.2
31	His-Phe-Arg-Trp-Gly-Lys-*Ser*-Val	32.3	25.5
32	His-DNle[[al]]-Arg-Trp-Gly-Lys-*Ser*-Val	73.9	25.0
33	His-Phe-Arg-Trp-Gly-Lys-*Phe*-Val	90.0	9.3
34	His-Phe-Arg-Trp-Gly-Lys-*DPhe*-Val	97.5	4.2
35	His-DPhe-Arg-Trp-Gly-Lys-*Phe*-Val	89.6	14.5
36	His-DPhe-Arg-Trp-Gly-Lys-*DPhe*-Val	82.0	24.9
37	His-DNle[[al]]-Arg-Trp-Gly-Lys-*Phe*-Val	99.7	0.6
38	His- DNle[[al]]-Arg-Trp-Gly-Lys-*DPhe*-Val	57.6	26.7
39	His-Phe-Arg-Trp-Gly-Lys-*Asp*-Val	5.9	9.1
40	His-Phe-Arg-Trp-Gly-Lys-*DAsp*-Val	15.7	15.6
41	His-DPhe-Arg-Trp-Gly-Lys-*Asp*-Val	3.7	4.9

42	His- DNle[[al]]-Arg-Trp-Gly-Lys-*Asp*-Val	16.8	22.3
43	His-Phe-Arg-Trp-Gly-Lys-*Glu*-Val	11.2	12.7
44	His- DNle[[al]]-Arg-Trp-Gly-Lys-*Glu*-Val	32.3	25.6
45	His-Phe-Arg-Trp-Gly-Lys-*Lys*-Val	41.0	26.9
46	His- DNle[[al]]-Arg-Trp-Gly-Lys-*Lys*-Val	85.4	26.1